

# #060

## Population Genomic Analyses Identify Signatures of Selection and Loci Associated with Agronomic Traits in Brassica Napus

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Brassica napus is one of the world's most valuable oilseed crops. Natural and artificial breeding selections of *B. napus* have resulted in numerous genetically diverse morphotypes and ecotypes with optimized traits and ecophysiological adaptation. To further understand the influence of selections on important agronomic traits, we conducted a comprehensive genomic assessment of genomic selection loci and their corresponding phenotypic traits based on the genome-wide resequencing of 800 diverse *B. napus* accessions. We detected 160 domestication-selective sweeps through comparisons of whole-genome genetic diversity between the different groups of oilseed rape accessions and between 120 loci associated with 30 agronomic traits after genome-wide association study (GWAS). There are 70 loci associated with 22 agronomic traits overlapped with selective sweeps. We found that six favourable alleles of low seed glucosinolate and erucic acid content, taken as examples, had been under strong selection in the process of 'double low' breeding (canola). Our results provide a genomic basis for improving *B. napus* cultivars and for further evolutionary analysis of oilseed crops.

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